

Table S1: Expression profile of the core set of genes altered by microbiota in the gut of Drosophila.

CG NUMBER	GENE SYMBOL	GENE FUNCTION	Effect of microbiota on:					
			young guts		old guts		DIRG ¹	GIRG ²
			Oregon R	Canton S	Canton S	CR/AX		
GENE EXPRESSION								
CG7670	WRNexo	3'-5' exonuclease activity	2.93	1.69	1.61	-	+	
CG6967	CG6967	nonsense-mediated decay	7.00	3.62	3.32	-	+	
CG31421	Takl1	MAP kinase kinase kinase activity	3.40	1.78	1.87	-	-	
CG15552	Sox100B	DNA bending activity	2.89	1.50	1.76	-	-	
CG17950	HmgD	DNA bending activity	2.13	1.34	1.49	-	+	
CG1070	Alh	sequence-specific DNA binding transcription factor activity	3.32	1.61	2.84	-	-	
CG12287	pdm2	specific RNA polymerase II transcription factor activity	3.06	1.34	2.16	-	-	
CG8337	E(spl)malpha	sequence-specific DNA binding	2.07	2.03	2.39	-	-	
CG6403	CG6403	chitin binding	-1.71	-1.30	-1.48	-	-	
CG15533	aSMase	sphingomyelin phosphodiesterase activity	-1.49	-1.37	-1.60	-	-	
GUT STRUCTURE								
CG3986	Cht4	chitinase activity	2.83	1.38	2.14	-	+	
CG33983	obst-H	chitin binding	2.42	1.31	2.64	-	-	
CG31901	Mur29B	chitin binding	2.75	1.70	1.78	-	-	
CG7017	CG7017	structural constituent of peritrophic membrane	1.59	1.39	2.03	-	+	
CG13586	itp	neuropeptide hormone activity	2.12	2.29	2.51	-	-	
CG1794	Mmp2	matrix metalloproteinase	2.26	1.99	3.59	-	+	
CG5730	AnniX	calcium-dependent phospholipid binding	2.06	1.31	1.58	+	+	
CG8095	scb	cell adhesion molecule binding	1.94	1.36	2.11	-	+	
CG3401	betaTub60D	structural constituent of cytoskeleton	4.51	2.72	3.12	-	+	
CG12051	Act42A	structural constituent of cytoskeleton	2.51	2.05	2.02	-	+	
CG9579	AnnX	actin binding	2.44	1.57	1.58	-	+	
CG31363	Jupiter	microtubule binding	1.93	1.61	1.77	-	+	
CG7293	Klp68D	motor activity	1.69	1.34	2.01	-	-	
CG8091	Nc	cell death	2.22	1.53	1.61	-	-	
CG9193	mus209	cell proliferation	2.49	1.73	1.45	-	+	
CG31453	pch2	ATP binding	2.48	1.89	1.86	-	+	
CG5940	CycA	cyclin	2.11	2.02	1.96	-	-	
CG11734	HERC2	ubiquitin protein ligase	1.47	1.38	2.09	-	-	
CG4700	Sema-2a	protein binding	2.10	1.66	1.92	-	-	
CG13521	robo	receptor activity	2.00	1.49	1.23	-	-	
IMMUNE RESPONSE								
CG7629	AttD	antimicrobial peptides	8.62	9.60	-1.12	+	+	
CG32279	dro2	antimicrobial peptides	5.78	4.13	4.76	-	+	
CG1385	Def	antimicrobial peptides	4.03	1.4	4.49	+	+	
CG10146	AttA	antimicrobial peptides	3.61	1.46	4.92	+	+	
CG18372	AttB	antimicrobial peptides	2.24	1.55	2.15	+	+	
CG32283	dro3	antimicrobial peptides	1.98	1.72	1.28	-	+	
CG9120	LysX	lysozyme	2.35	3.34	2.86	-	+	
CG31508	TotC	Turandots	1.47	1.53	-1.16	-	+	
CG31509	TotA	Turandots	1.40	2.78	-1.05	-	+	
CG7496	PGRP-SD	imd	2.51	2.71	2.31	+	+	
CG16910	key	imd	2.05	1.41	1.41	-	+	
CG8577	PGRP-SC1a/b	imd	1.33	2.18	-1.40	+	+	
METABOLISM/DIGESTION								
CG3074	dmw	peptidase	3.51	1.62	3.56	-	+	
CG30090	CG30090	serine-type endopeptidase activity	3.28	2.24	1.84	-	+	
CG4445	pgant3	polypeptide N-acetylgalactosaminyltransferase activity	3.05	1.68	2.35	-	+	
CG31410	Npc2e	sterol transport	2.65	1.59	3.34	-	+	
CG4799	Pen	protein transmembrane transporter activity	2.55	2.13	2.31	-	+	
CG3181	Ts	thymidylate synthase activity	2.53	1.40	1.51	-	+	
CG1220	Kaz1-ORFB	serine-type endopeptidase inhibitor activity	2.49	1.51	1.83	-	-	
CG6869	FucTA	fucosyl transferase	2.48	1.52	2.29	-	+	
CG8975	RnrS	ribonucleoside-diphosphate reductase activity	2.31	1.68	1.40	-	+	
CG4998	CG4998	serine-type endopeptidase activity	2.25	3.17	6.98	-	-	
CG5518	sda	aminopeptidase activity	2.25	1.50	2.00	-	+	
CG15829	CG15829	fatty-acyl-CoA binding	2.20	2.72	3.62	+	+	
CG10559	CG10559	transferase activity, transferring phosphorus-containing groups	2.16	1.39	-1.02	-	+	
CG32684	alpha-Man-I	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity	2.06	1.48	1.72	-	+	
CG5371	RnrL	ribonucleoside-diphosphate reductase activity	2.06	1.46	1.33	-	+	
CG18188	Damm	cysteine-type endopeptidase activity	1.98	1.30	1.75	-	+	
CG8066	CG8066	homology cysteine-type endopeptidase inhibitor activity	1.91	1.33	1.63	-	-	
CG10178	CG10178	glucuronosyltransferase activity	1.87	2.00	3.13	-	+	
CG31216	Naam	nicotinamidase activity	1.82	1.59	2.00	-	+	
CG4860	CG4860	acyl-CoA dehydrogenase activity	1.77	1.44	1.38	-	-	
CG17191	CG17191	triglyceride lipase activity	1.75	1.62	2.96	-	-	
CG7291	Npc2a	sterol binding	1.69	1.44	1.61	-	-	
CG15695	CG15695	catalytic activity	1.66	1.82	1.21	-	-	

CG9360	CG9360	Glucose/ribitol dehydrogenase; NAD(P)-binding domain	1.64	1.84	-1.25	+	-
CG7118	Jon66Ci	serine-type endopeptidase activity	1.56	2.12	1.04	-	+
CG10126	CG10126	calcium ion binding	1.55	1.48	1.43	-	+
CG31148	CG31148	glucosylceramidase activity	1.32	1.45	1.83	-	+
CG17636	CG17636	gamma-glutamyltransferase activity	-1.41	-1.32	1.00	-	-
CG17192	CG17192	phospholipase A1 activity	-1.48	-1.34	-2.08	+	+
CG14606	CG14606	hexose transmembrane transporter activity	-1.48	-1.58	-1.63	-	+
CG17167	CG17167	calcium, potassium:sodium symporter activity	-1.51	-1.31	-1.28	-	-
CG14205	CG14205	unknown	-1.61	-1.32	-1.09	-	+
CG8358	CG8358	metalloendopeptidase activity	-1.67	-1.37	-1.05	+	-
CG31089	CG31089	triacylglycerol lipase activity	-1.68	-1.42	-2.29	-	+
CG14694	CG14694	folic acid binding / metabolism of vitamins and co-factors	-1.73	-1.41	-1.83	-	-
CG1082	alpha-Est4	carboxylesterase activity	-1.85	-1.32	-1.58	-	+
CG10182	CG10182	unknown	-1.89	-1.36	-1.7	-	+
CG3747	Eaat1	glutamate/sodium symporter activity	-1.89	-1.33	-1.18	-	+
CG7923	Fad2	Fatty acid desaturase	-1.94	-1.31	-1.49	-	-
CG6296	CG6296	phospholipase A1 activity	-2.01	-1.35	-1.68	-	-
CG9465	CG9465	alphamannosidase activity	-2.11	-1.32	-1.83	-	+
CG6898	Zip3	metal ion transporter activity	-2.21	-1.34	-1.4	+	-
CG31091	CG31091	triacylglycerol lipase activity	-2.39	-1.38	-2.56	-	+
CG32751	CG32751	pantheninase hydrolase activity	-2.51	-1.42	-2.29	-	+
CG9825	CG9825	high affinity inorganic phosphate:sodium symporter activity	-2.91	-1.46	-1.41	-	+
CG31783	ninaD	carotenoid transport	-3.06	-1.39	-2.57	-	+
SIGNALING							
CG15154	Socs36E	JAK-STAT pathway	2.34	1.71	2.15	-	+
CG5963	upd3	JAK-STAT pathway	1.66	1.61	2.22	-	+
CG3619	DI	Notch pathway	2.30	1.60	1.50	+	+
CG10580	fng	Notch pathway	1.97	1.37	1.50	-	+
CG8346	HLHm3	Notch pathway	1.89	1.41	1.53	-	-
CG9670	fal	other pathways	2.55	1.73	1.84	-	-
CG7103	Pvf1	PVF pathway	6.50	2.15	2.50	-	+
CG13388	Akap200	transduction/modulation	2.72	1.82	2.52	-	+
CG2699	Pi3K21B	transduction/modulation	2.45	1.79	2.13	-	-
CG16987	daw	transforming growth factor beta receptor signaling pathway	-3.08	-1.59	-1.49	-	-
STRESS RESPONSE							
CG14031	Cyp4ac3	cytochrome P450	1.44	1.30	1.34	-	-
CG4463	Hsp23	HSP	3.39	15.29	4.54	-	+
CG18743	Hsp70Ab	HSP	3.08	3.62	3.64	-	+
CG6489	Hsp70Bc	HSP	2.25	1.86	1.51	+	+
CG6489	Hsp70Ba/Bb/Bbb/Bc	HSP	2.72	2.13	2.00	+	+
CG32041	Hsp22 /// Hsp67Bb	HSP	1.88	2.74	-1.04	-	-
CG4183	Hsp26	HSP	1.70	3.33	1.86	-	+
CG4466	Hsp27	HSP	1.56	2.86	1.98	-	+
CG12242	GstD5	glutathione transferase activity	1.59	1.42	-1.13	-	+
CG4421	GstD8	glutathione transferase activity	1.57	1.42	1.50	-	+
CG3540	Cyp4d14	cytochrome P450	-1.38	-1.36	-1.74	+	+
CG3972	Cyp4g1	cytochrome P450	-4.10	-1.66	-2.34	-	-
CG8523	Mdr50	substance transmembrane transporter activity	-2.33	-1.45	-1.82	-	+
CG4371	GstD7	glutathione transferase activity	-1.47	-1.30	-2.04	-	+
UNKNOWN GENES							
CG42807	CG42807	unknown peptide	15.55	22.70	7.02	-	+
CG32368	CG32368	unknown peptide	13.35	4.73	3.49	-	+
CG12970	CG12970	-	7.71	4.68	5.84	-	+
CG8353	CG8353	-	6.72	3.13	2.22	-	+
CG4250	CG4250	unknown peptide	5.75	3.32	8.46	+	-
CG15199	CG15199	-	5.13	5.00	1.91	-	+
CG6640	CG6640	-	4.51	3.79	2.95	-	+
CG16995	CG16995	unknown peptide	4.16	2.03	1.40	-	+
CG14499	CG14499	unknown peptide	4.11	3.02	1.66	-	-
CG14696	CG14696	-	3.99	1.92	1.91	-	-
CG5118	CG5118	-	3.43	1.87	1.98	+	-
CG31344	CG31344	-	3.09	1.79	1.55	-	+
CG33468	CG33468	unknown peptide	2.98	1.45	1.33	-	+
CG10943	CG10943	unknown peptide	2.89	1.45	1.44	-	+
CG5910	CG5910	-	2.57	1.38	1.42	-	+
CG5630	CG5630	-	2.55	2.02	2.34	-	+
CG11671	CG11671	unknown peptide	2.52	1.51	1.39	-	+
CG15210	CG15210	unknown peptide	2.48	1.39	1.81	-	+
CG4269	CG4269	-	2.43	2.71	1.32	+	+
CG13117	CG13117	-	2.42	1.36	2.78	-	-
CG34236	CG34236	unknown peptide	2.26	1.51	1.64	-	-
CG13488	CG13488	unknown peptide	2.25	1.89	2.26	-	+
CG11141	CG11141	-	2.24	1.38	1.54	-	+
CG13190	cuff	-	2.20	1.63	2.31	-	-

CG30154	CG30154	unknown peptide	2.05	1.84	1.78	-	+
CG14872	CG14872	unknown peptide	2.03	2.58	1.50	-	+
CG15083	CG15083	-	1.72	1.53	1.95	-	+
CG4716	CG4716	-	1.60	1.42	1.02	+	-
CG18067	CG18067	unknown peptide	1.57	1.40	1.31	+	+
CG11885	CG11885	unknown peptide	1.52	1.54	1.59	-	-
CG14872	CG14872	binding	1.50	1.44	1.50	-	+
CG14872	CG14872	binding	1.45	1.33	1.42	-	+
CG40271	CG40271	-	1.41	1.33	1.28	-	-
CG10102	CG10102	binding	1.37	1.53	-1.12	-	+
CG8317	CG8317	-	1.33	1.31	-1.34	-	+
CG6749	CG6749	-	-1.31	-1.35	-1.07		
CG15213	CG15213	-	-1.58	-1.43	-1.12	-	-
CG16904	CG16904	-	-1.83	-1.32	-1.23	-	-
CG30008	CG30008	-	-1.96	-1.32	-1.26	-	-
CG32407	CG32407	-	-2.04	-1.40	-1.95	-	+

¹ de Gregorio E, Spellman PT, Rubin GM, Lemaitre B. 2001. Genome-wide analysis of the *Drosophila* immune response by using oligonucleotide microarrays. Proc Natl Acad Sci USA 98:12590–12595.

² Buchon N, Broderick NA, Poidevin M, Pradervand S, Lemaitre B. 2009. *Drosophila* intestinal response to bacterial infection: activation of host defense and stem cell proliferation. Cell Host Microbe 5:200–211.

